

III. AMENDMENT TO THE SEQUENCE LISTING

Please replace the Sequence Listing currently on record with the substitute Sequence Listing enclosed herewith.



SEQUENCE LISTING

<110> ~~DAUGERSON~~, DARRELL R.HANNA, NABIL
BRAMS, PETER
HEARD, CHERYL<120> INDENTIFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN
CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2
CO-STIMULATORY ANTIGENS

<130> 37003-280705

<140> 10/073138

<141> 2002-02-13

<150> PCT/US97/19906

<151> 1997-10-29

<150> 08/746,361

<151> 1996-11-08

<150> 08/487,550

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<170> PatentIn Ver. 2.1

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Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys	
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Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln	
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 Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ala Ala Ser Leu Ala Ile
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acc	gtg	gag	aag	aca	gtg	gcc	cct	aca	gaa	tgt	tca	tga				711	
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Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp		
1				5					10					15			
gtc	ctg	tcc	cag	gtg	cag	ctg	cag	gag	tgc	ggc	cca	gga	ctg	gtg	aag	96	
Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys		
			20					25					30				
cct	tgc	gag	acc	ctg	tcc	ctc	acc	tgc	gct	gtc	tct	ggt	ggc	tcc	atc	144	
Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Ala	Val	Ser	Gly	Gly	Ser	Ile		
		35					40					45					
agc	ggt	ggt	tat	ggc	tgg	ggc	tgg	atc	cgc	cag	ccc	cca	ggg	aag	ggg	192	
Ser	Gly	Gly	Tyr	Gly	Trp	Gly	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly		
	50					55					60						
ctg	gag	tgg	att	ggg	agt	ttc	tat	agt	agt	agt	ggg	aac	acc	tac	tac	240	
Leu	Glu	Trp	Ile	Gly	Ser	Phe	Tyr	Ser	Ser	Ser	Gly	Asn	Thr	Tyr	Tyr		
	65				70				75					80			
aac	ccc	tcc	ctc	aag	agt	caa	gtc	acc	att	tca	aca	gac	acg	tcc	aag	288	
Asn	Pro	Ser	Leu	Lys	Ser	Gln	Val	Thr	Ile	Ser	Thr	Asp	Thr	Ser	Lys		
			85						90					95			
aac	cag	ttc	tcc	ctg	aag	ctg	aac	tct	atg	acc	gcc	gcg	gac	acg	gcc	336	
Asn	Gln	Phe	Ser	Leu	Lys	Leu	Asn	Ser	Met	Thr	Ala	Ala	Asp	Thr	Ala		
			100				105						110				
gtg	tat	tac	tgt	gtg	aga	gat	cgt	ctt	ttt	tca	gtt	gtt	gga	atg	gtt	384	
Val	Tyr	Tyr	Cys	Val	Arg	Asp	Arg	Leu	Phe	Ser	Val	Val	Gly	Met	Val		
		115					120					125					
tac	aac	aac	tgg	ttc	gat	gtc	tgg	ggc	ccg	gga	gtc	ctg	gtc	acc	gtc	432	
Tyr	Asn	Asn	Trp	Phe	Asp	Val	Trp	Gly	Pro	Gly	Val	Leu	Val	Thr	Val		
	130					135					140						

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Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser	
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Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys	
165 170 175	
gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg	576
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu	
180 185 190	
acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc	624
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu	
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tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc	672
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr	
210 215 220	
cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg	720
Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val	
225 230 235 240	
gac aag aaa gca gag ccc aaa tct tgt gac aaa act cac aca tgc cca	768
Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro	
245 250 255	
ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc	816
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe	
260 265 270	
ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc	864
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val	
275 280 285	
aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc	912
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe	
290 295 300	
aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg	960
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro	
305 310 315 320	
cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc	1008
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr	
325 330 335	
gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc	1056
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val	
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tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc	1104
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala	
355 360 365	
aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg	1152
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg	
370 375 380	

gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc	1200
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly	
385 390 395 400	
ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg	1248
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro	
405 410 415	
gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc	1296
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser	
420 425 430	
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Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln	
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ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac	1392
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His	
450 455 460	
tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga	1431
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys	
465 470 475	